IN THE CLAIMS

Please replace the pending claims with the correspondingly numbered claims below. Claims amended herein are noted by the text in parentheses. Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment; captioned "VERSION WITH MARKINGS TO SHOW CHANGES MADE."

26. (currently amended) A method for identifying ~~in vitro screening for~~ a target molecule that binds to a transdominant intracellular bioactive ~~agent~~ peptide capable of altering the phenotype of a cell, said method comprising the steps:

a) introducing a molecular library comprising different nucleic acid sequences ~~of randomized candidate nucleic acids~~ into a plurality of cells, wherein said nucleic acid sequences each comprise a sequence encoding a candidate randomized bioactive peptide of from 4 to 100 amino acids in length, ~~wherein each of said nucleic acids comprises a different nucleotide sequence, wherein said randomized candidate nucleic acids are expressed in said cells to produce a plurality of randomized peptides~~, and wherein said nucleic acid sequences are expressed in said cells to produce a plurality of randomized bioactive peptides;

b) screening said plurality of cells for a cell exhibiting an altered phenotype, wherein said altered phenotype is due to the presence of a transdominant bioactive peptide ~~agent; and~~

c) identifying a target molecule to which said transdominant bioactive agent binds.

27. (currently amended) A method according to claim 26 wherein said identifying comprises:

(i) isolating said cell exhibiting an altered phenotype;

(ii) isolating said transdominant bioactive peptide; and

(iii) binding said transdominant bioactive agent to said target to identify said target.

28. (currently amended) A method according to claim 26 further comprising the step:

d) isolating a target molecule using

i) said ~~candidate nucleic acid~~ nucleic acid sequences; or

ii) ~~the expression product of said candidate nucleic acid~~ said randomized bioactive peptides.

29. (currently amended) A method according to claim 26 wherein said nucleic acid sequences further ~~comprise~~ encode a presentation structure ~~sequence~~ capable of presenting said ~~expression product~~ randomized bioactive peptides in a conformationally restricted form.

30. (previously amended) A method according to claim 26 wherein said introducing is with retroviral vectors.

31. (previously amended) A method according to claim 26 wherein said cells are mammalian cells.

32. (previously amended) A method according to claim 26 wherein said library comprises at least 10^4 different nucleic acids.

33. (previously amended) A method according to claim 26 wherein said library comprises at least 10^5 different nucleic acids.

34. (previously amended) A method according to claim 26 wherein said library comprises at least 10^6 different nucleic acids.

35. (previously amended) A method according to claim 26 wherein said library comprises at least 10^7 different nucleic acids.

36. (previously amended) A method according to claim 26 wherein said library comprises at least 10^8 different nucleic acids.

37. (previously amended) A method according to claim 26 wherein each of said candidate nucleic acids is linked to nucleic acid encoding at least one fusion partner.

38. (canceled)